

03C6 / 0590
0321 #7



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RAW SEQUENCE LISTING

DATE: 03/13/2002

PATENT APPLICATION: US/09/855,266A

TIME: 11:51:31

Input Set : A:\06501-040002.txt

Output Set: N:\CRF3\03132002\I855266A.raw

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4 <110> APPLICANT: Kimura, Naoki
5   Toyoshima, Tomoko
7 <120> TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
9 <130> FILE REFERENCE: 06501-040002
11 <140> CURRENT APPLICATION NUMBER: US 09/855,266A
12 <141> CURRENT FILING DATE: 2001-05-14
14 <150> PRIOR APPLICATION NUMBER: US 09/411,722
15 <151> PRIOR FILING DATE: 1999-10-01
17 <150> PRIOR APPLICATION NUMBER: PCT/JP98/01511
18 <151> PRIOR FILING DATE: 1998-04-01
20 <150> PRIOR APPLICATION NUMBER: JP 9/099653
21 <151> PRIOR FILING DATE: 1997-04-01
23 <160> NUMBER OF SEQ ID NOS: 13
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 176
29 <212> TYPE: PRT
30 <213> ORGANISM: Mus musculus
32 <400> SEQUENCE: 1
33 Met Val Thr Phe Ser His Val Ser Ser Leu Ser His Trp Phe Leu Leu
34   1               5               10               15
35 Leu Leu Leu Leu Asn Leu Phe Leu Pro Val Ile Phe Ala Met Pro Glu
36   20               25               30
37 Ser Tyr Ser Phe Asn Cys Pro Asp Gly Glu Tyr Gln Ser Asn Asp Val
38   35               40               45
39 Cys Cys Lys Thr Cys Pro Ser Gly Thr Phe Val Lys Ala Pro Cys Lys
40   50               55               60
41 Ile Pro His Thr Gln Gly Gln Cys Glu Lys Cys His Pro Gly Thr Phe
42   65               70               75               80
43 Thr Gly Lys Asp Asn Gly Leu His Asp Cys Glu Leu Cys Ser Thr Cys
44   85               90               95
45 Asp Lys Asp Gln Asn Met Val Ala Asp Cys Ser Ala Thr Ser Asp Arg
46   100              105              110
47 Lys Cys Glu Cys Gln Ile Gly Leu Tyr Tyr Tyr Asp Pro Lys Phe Pro
48   115              120              125
49 Glu Ser Cys Arg Pro Cys Thr Lys Cys Pro Gln Gly Ile Pro Val Leu
50   130              135              140
51 Gln Glu Cys Asn Ser Thr Ala Asn Thr Val Cys Ser Ser Ser Val Ser
52   145              150              155              160
53 Asn Pro Arg Asn Trp Leu Phe Leu Leu Met Leu Ile Val Phe Cys Ile
54   165              170              175
56 <210> SEQ ID NO: 2
57 <211> LENGTH: 148

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58 <212> TYPE: PRT
59 <213> ORGANISM: Mus musculus
61 <400> SEQUENCE: 2
62 Ala Met Pro Glu Ser Tyr Ser Phe Asn Cys Pro Asp Gly Glu Tyr Gln
63   1           5           10           15
64 Ser Asn Asp Val Cys Cys Lys Thr Cys Pro Ser Gly Thr Phe Val Lys
65           20           25           30
66 Ala Pro Cys Lys Ile Pro His Thr Gln Gly Gln Cys Glu Lys Cys His
67           35           40           45
68 Pro Gly Thr Phe Thr Gly Lys Asp Asn Gly Leu His Asp Cys Glu Leu
69           50           55           60
70 Cys Ser Thr Cys Asp Lys Asp Gln Asn Met Val Ala Asp Cys Ser Ala
71   65           70           75           80
72 Thr Ser Asp Arg Lys Cys Glu Cys Gln Ile Gly Leu Tyr Tyr Tyr Asp
73           85           90           95
74 Pro Lys Phe Pro Glu Ser Cys Arg Pro Cys Thr Lys Cys Pro Gln Gly
75           100          105          110
76 Ile Pro Val Leu Gln Glu Cys Asn Ser Thr Ala Asn Thr Val Cys Ser
77           115          120          125
78 Ser Ser Val Ser Asn Pro Arg Asn Trp Leu Phe Leu Leu Met Leu Ile
79           130          135          140
80 Val Phe Cys Ile
81 145
83 <210> SEQ ID NO: 3
84 <211> LENGTH: 1509
85 <212> TYPE: DNA
86 <213> ORGANISM: Mus musculus
88 <220> FEATURE:
89 <221> NAME/KEY: CDS
90 <222> LOCATION: (12)...(539)
92 <400> SEQUENCE: 3
93 agctcacagc c atg gtt acc ttc agc cac gtc tcc agt ctg agt cac tgg      50
94           Met Val Thr Phe Ser His Val Ser Ser Leu Ser His Trp
95           1           5           10
97 ttc ctc ttg ctg ctg ctg aat ctg ttc ttg ccg gta ata ttt gct      98
98 Phe Leu Leu Leu Leu Leu Leu Asn Leu Phe Leu Pro Val Ile Phe Ala
99           15           20           25
101 atg cct gaa tca tac tcc ttc aac tgt ccc gat ggt gaa tac cag tct      146
102 Met Pro Glu Ser Tyr Ser Phe Asn Cys Pro Asp Gly Glu Tyr Gln Ser
103   30           35           40           45
105 aat gat gtc tgt tgc aag acc tgt ccc tca ggt aca ttt gtc aag gcg      194
106 Asn Asp Val Cys Cys Lys Thr Cys Pro Ser Gly Thr Phe Val Lys Ala
107           50           55           60
109 ccc tgc aaa atc ccc cat act caa gga caa tgt gag aag tgt cac cca      242
110 Pro Cys Lys Ile Pro His Thr Gln Gly Gln Cys Glu Lys Cys His Pro
111           65           70           75
113 gga aca ttc aca ggg aaa gat aat ggc ctg cat gat tgt gaa ctt tgc      290
114 Gly Thr Phe Thr Gly Lys Asp Asn Gly Leu His Asp Cys Glu Leu Cys
115           80           85           90

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117 tcc acc tgt gat aaa gac cag aat atg gtg gct gac tgt tct gcc acc      338
118 Ser Thr Cys Asp Lys Asp Gln Asn Met Val Ala Asp Cys Ser Ala Thr
119      95                      100                      105
121 agt gac cgg aaa tgc gag tgc caa ata ggt ctt tac tac tat gac cca      386
122 Ser Asp Arg Lys Cys Glu Cys Gln Ile Gly Leu Tyr Tyr Tyr Asp Pro
123 110                      115                      120                      125
125 aaa ttt ccg gaa tca tgc cgc cca tgt acc aag tgt ccc caa gga atc      434
126 Lys Phe Pro Glu Ser Cys Arg Pro Cys Thr Lys Cys Pro Gln Gly Ile
127                      130                      135                      140
129 cct gtc ctc cag gaa tgc aac tcc aca gct aac act gtg tgc agt tca      482
130 Pro Val Leu Gln Glu Cys Asn Ser Thr Ala Asn Thr Val Cys Ser Ser
131                      145                      150                      155
133 tct gtt tca aat ccc aga aac tgg ctg ttc cta ctg atg cta att gtc      530
134 Ser Val Ser Asn Pro Arg Asn Trp Leu Phe Leu Leu Met Leu Ile Val
135                      160                      165                      170
137 ttc tgt atc tgaagaagat aaagggttcta cagatgggtgt ctgtagcttc      579
138 Phe Cys Ile
139      175
141 cttttattgc tgtgaagaga aaccatggag gcaactcttt cattttatctt tatttttttaa      639
142 tgtcttgaac ttgatttgaa gaccaggctg gactcaaaact cacagagatc cggactaggc      699
143 acctctaata taggaaaaca ttgaattggg actggcttac agtttcagaa gttctgtcca      759
144 tgattatcat agtgcgaagc atggaggcac ggaggcacac atggtgctgg agaagaagct      819
145 gagagttctg catcttgatc tgcaagcaat aaaaggagac tgtgtgccac actacacata      879
146 gcttgaacat aggagacctc aaagcctgtc cccacagtga caaacttcct ccaacaaggt      939
147 catacctcct aataatacca tttcttatga ggcaagcatt caaacacatg agtctatgag      999
148 ggccaaacca attcaaacca ccacagggtta acaattgccc tctgcagctc tctggtggag      1059
149 gccctccttg agagtaagta acaatttaga tgaaggcaag tcctgggtatc aggtccaaaa      1119
150 gaaactcagg atgaatggtc cactgtgggt cctattaaca tactgaagaa catgacctca      1179
151 ccttagactt ctccacctca ctggcttccc ttcccctagc ttctcattcc caggtaaccc      1239
152 tgccattttt tggtaatgtg ccttcttggg tcttctctc ctttcccct ctctctgtg      1299
153 ccttattttct ctctctctcc cactctccac cagccgcctc ttaaggcctg agtcagtctg      1359
154 caggccatgt ttaatctact actttctctc tgcctctggac tcatccagat gtctctggct      1419
155 gagctctccc tctatctac aataaaacct tcccctaac cagaaatgga acagttttgt      1479
156 cctcactttg tacatctggt gctgaaacc      1509
158 <210> SEQ ID NO: 4
159 <211> LENGTH: 43
160 <212> TYPE: DNA
161 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
164 <223> OTHER INFORMATION: Synthetically generated primer
166 <400> SEQUENCE: 4
167 gcgccgcgca attctgacta actgacgggg gggggggggg ggg      43
169 <210> SEQ ID NO: 5
170 <211> LENGTH: 26
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial Sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: Synthetically generated primer
177 <400> SEQUENCE: 5

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178 ccgcgagctc gatatcaagc ttgtac                                     26
180 <210> SEQ ID NO: 6
181 <211> LENGTH: 29
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: Synthetically generated primer
188 <400> SEQUENCE: 6
189 ggcgctcgag ctatagttcg aacatggag                                     29
191 <210> SEQ ID NO: 7
192 <211> LENGTH: 29
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <223> OTHER INFORMATION: Synthetically generated primer
199 <400> SEQUENCE: 7
200 gaggtacaag cttgatatcg agctcgcgg                                     29
202 <210> SEQ ID NO: 8
203 <211> LENGTH: 23
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: Synthetically generated primer
210 <400> SEQUENCE: 8
211 gccgcgaatt ctgactaact gac                                         23
213 <210> SEQ ID NO: 9
214 <211> LENGTH: 24
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Synthetically generated primer
221 <400> SEQUENCE: 9
222 ggatccttca actgtcccga tggc                                         24
224 <210> SEQ ID NO: 10
225 <211> LENGTH: 26
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Synthetically generated primer
232 <400> SEQUENCE: 10
233 gaattccaca cagtgttagc tgtgga                                       26
235 <210> SEQ ID NO: 11
236 <211> LENGTH: 36
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Synthetically generated primer
243 <400> SEQUENCE: 11
244 ccgaattcca ccatggttac cttcagccac gtctcc                           36

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246 <210> SEQ ID NO: 12
247 <211> LENGTH: 35
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: Synthetically generated primer
254 <400> SEQUENCE: 12
255 ccggatcctc agatacagaa gacaattagc atcag
257 <210> SEQ ID NO: 13
258 <211> LENGTH: 123
259 <212> TYPE: PRT
260 <213> ORGANISM: Mus musculus
262 <400> SEQUENCE: 13
263 Cys Pro Gly Gly Lys Tyr Val His Ser Lys Asn Asn Ser Ile Cys Cys
264 1 5 10 15
265 Thr Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro
266 20 25 30
267 Gly Arg Asp Thr Val Cys Arg Glu Cys Glu Lys Gly Thr Phe Thr Ala
268 35 40 45
269 Ser Gln Asn Tyr Leu Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys
270 50 55 60
271 Glu Met Ser Gln Val Glu Ile Ser Pro Cys Gln Ala Asp Lys Asp Thr
272 65 70 75 80
273 Val Cys Gly Cys Lys Glu Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr
274 85 90 95
275 His Phe Gln Cys Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr
276 100 105 110
277 Ile Pro Cys Lys Glu Thr Gln Asn Thr Val Cys
278 115 120

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VERIFICATION SUMMARY

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